

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 101521,109  
Source: PCT  
Date Processed by STIC: 1-27-05

***ENTERED***

## CRF ERRORS Edited By the STIC Systems Branch

Serial Number: 101521,109

CRF Edit Date: 1-27-05  
Edited by: KE

Realigned nucleic acid/amino acid numbers/text: increases where the sequence text "wrapped" to the next line

Corrected the SEQ ID NO. Sequence numbers edited were:

Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

Deleted:  invalid beginning/end-of-file text;  page numbers

Inserted mandatory headings/numeric identifiers, specifically:

Moved responses to same line as heading/numeric identifier, specifically:

Other:



PCT

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/521,109

DATE: 01/27/2005  
TIME: 09:43:17

Input Set : A:\pto.kd.txt  
Output Set: N:\CRF4\01272005\J521109.raw

3 <110> APPLICANT: TEDESCO, Francesco  
4 MARZARI, Roberto  
6 <120> TITLE OF INVENTION: Antibodies anti C5 of the complement and their use  
8 <130> FILE REFERENCE: 50294/016001  
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/521,109  
C--> 10 <141> CURRENT FILING DATE: 2005-01-11  
10 <150> PRIOR APPLICATION NUMBER: PCT/EP2003/007487  
11 <151> PRIOR FILING DATE: 2003-07-10  
13 <150> PRIOR APPLICATION NUMBER: MI2002A001527  
14 <151> PRIOR FILING DATE: 2002-07-11  
16 <160> NUMBER OF SEQ ID NOS: 35  
18 <170> SOFTWARE: PatentIn version 3.1  
20 <210> SEQ ID NO: 1  
21 <211> LENGTH: 342  
22 <212> TYPE: DNA  
23 <213> ORGANISM: Homo sapiens  
25 <220> FEATURE:  
26 <221> NAME/KEY: CDS  
27 <222> LOCATION: (1)..(342)  
28 <223> OTHER INFORMATION: Light chain of the TS-A12/22 antibody  
31 <400> SEQUENCE: 1  
32 gac atc cgg atg acc cag tct cca gac tcc ctg gct gtg tct ctg ggc 48  
33 Asp Ile Arg Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly  
34 1 5 10 15  
36 gag agg gcc acc atc aac tgc aag tcc agc cag agt gtt tta tac agc 96  
37 Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser  
38 20 25 30  
40 tcc aac aat aag aac tac tta gct tgg tac cag cag aaa cca gga cag 144  
41 Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln  
42 35 40 45  
44 cct cct aag ctc att tac tgg gca tct acc cgg gaa tcc ggg gtc 192  
45 Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val  
46 50 55 60  
48 cct gac cga ttc agt ggc agc ggg tct ggg aca gat ttc act ctc acc 240  
49 Pro Asp Arg Phe Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr  
50 65 70 75 80  
52 atc agc agc ctg cag gct gaa gat gtg gca gtt tat tac tgt cag caa 288  
53 Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln  
54 85 90 95  
56 tat tat agt act cct cag ctc act ttc ggc gga agg acc aaa gtg gat 336  
57 Tyr Tyr Ser Thr Pro Gln Leu Thr Phe Gly Gly Arg Thr Lys Val Asp  
58 100 105 110  
60 atc aaa 342

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61 Ile Lys  
 65 <210> SEQ ID NO: 2  
 66 <211> LENGTH: 114  
 67 <212> TYPE: PRT  
 68 <213> ORGANISM: Homo sapiens  
 70 <400> SEQUENCE: 2  
 72 Asp Ile Arg Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly  
 73 1 5 10 15  
 76 Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser  
 77 20 25 30  
 80 Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln  
 81 35 40 45  
 84 Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val  
 85 50 55 60  
 88 Pro Asp Arg Phe Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr  
 89 65 70 75 80  
 92 Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln  
 93 85 90 95  
 96 Tyr Tyr Ser Thr Pro Gln Leu Thr Phe Gly Gly Arg Thr Lys Val Asp  
 97 100 105 110  
 100 Ile Lys  
 104 <210> SEQ ID NO: 3  
 105 <211> LENGTH: 345  
 106 <212> TYPE: DNA  
 107 <213> ORGANISM: Homo sapiens  
 109 <220> FEATURE:  
 110 <221> NAME/KEY: CDS  
 111 <222> LOCATION: (1)..(345)  
 112 <223> OTHER INFORMATION: Heavy chain of the TS-A12/22 antibody  
 115 <400> SEQUENCE: 3  
 116 cag gta cag ctg cag cag tca gag gga ggc gtg gtc cag cct ggg agg 48  
 117 Gln Val Gln Leu Gln Gln Ser Glu Gly Gly Val Val Gln Pro Gly Arg  
 118 1 5 10 15  
 120 tcc ctg aga ctc tcc tgt gca gcg tct gga ttc acc ttc agt agc tat 96  
 121 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr  
 122 20 25 30  
 124 ggc atg aac tgg gtc cgc cag gct cca ggg aag ggg ctg gag tgg gtt 144  
 125 Gly Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 126 35 40 45  
 128 tca tac att agt agt agt agt acc ata tac tac gca gac tct gtg 192  
 129 Ser Tyr Ile Ser Ser Ser Thr Ile Tyr Tyr Ala Asp Ser Val  
 130 50 55 60  
 132 aag ggc cga ttc acc atc tcc aga gac aat tcc aag aac acg ctg tat 240  
 133 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
 134 65 70 75 80  
 136 ctg caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac tgt 288  
 137 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 138 85 90 95  
 140 gcg aga ggg cct ggt atg gac gtc tgg ggc caa ggg acc acg gtc acc 336

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Input Set : A:\pto.kd.txt

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141 Ala Arg Gly Pro Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr  
 142 100 105 110 345  
 144 gtc tcc tca  
 145 Val Ser Ser  
 146 115  
 149 <210> SEQ ID NO: 4  
 150 <211> LENGTH: 115  
 151 <212> TYPE: PRT  
 152 <213> ORGANISM: Homo sapiens  
 154 <400> SEQUENCE: 4  
 156 Gln Val Gln Leu Gln Gln Ser Glu Gly Gly Val Val Gln Pro Gly Arg  
 157 1 5 10 15  
 160 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr  
 161 20 25 30  
 164 Gly Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 165 35 40 45  
 168 Ser Tyr Ile Ser Ser Ser Ser Thr Ile Tyr Tyr Ala Asp Ser Val  
 169 50 55 60  
 172 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
 173 65 70 75 80  
 176 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 177 85 90 95  
 180 Ala Arg Gly Pro Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr  
 181 100 105 110  
 184 Val Ser Ser  
 185 115  
 188 <210> SEQ ID NO: 5  
 189 <211> LENGTH: 750  
 190 <212> TYPE: DNA  
 191 <213> ORGANISM: Homo sapiens  
 193 <220> FEATURE:  
 194 <221> NAME/KEY: CDS  
 195 <222> LOCATION: (1)..(750)  
 196 <223> OTHER INFORMATION: scFv  
 199 <400> SEQUENCE: 5  
 200 gac atc cgg atg acc cag tct cca gac tcc ctg gct gtg tct ctg ggc 48  
 201 Asp Ile Arg Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly  
 202 1 5 10 15  
 204 gag agg gcc acc atc aac tgc aag tcc agc cag agt gtt tta tac agc 96  
 205 Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser  
 206 20 25 30  
 208 tcc aac aat aag aac tac tta gct tgg tac cag cag aaa cca gga cag 144  
 209 Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln  
 210 35 40 45  
 212 cct cct aag ctg ctc att tac tgg gca tct acc cgg gaa tcc ggg gtc 192  
 213 Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val  
 214 50 55 60  
 216 cct gac cga ttc agt ggc agc ggg tct ggg aca gat ttc act ctc acc 240  
 217 Pro Asp Arg Phe Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr

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218	65	70	75	80													
220	atc	agc	agc	ctg	cag	gct	gaa	gat	gtg	gca	gtt	tat	tac	tgt	cag	caa	288
221	Ile	Ser	Ser	Leu	Gln	Ala	Glu	Asp	Val	Ala	Val	Tyr	Tyr	Cys	Gln	Gln	
222																95	
224	tat	tat	agt	act	cct	cag	ctc	act	ttc	ggc	gga	agg	acc	aaa	gtg	gat	336
225	Tyr	Tyr	Ser	Thr	Pro	Gln	Leu	Thr	Phe	Gly	Gly	Arg	Thr	Lys	Val	Asp	
226																110	
228	atc	aaa	tcc	gga	ggg	tcg	acc	ata	act	tcg	tat	aat	gta	tac	tat	acg	384
229	Ile	Lys	Ser	Gly	Gly	Ser	Thr	Ile	Thr	Ser	Tyr	Asn	Val	Tyr	Tyr	Thr	
230																125	
232	aag	tta	tcc	tcg	agc	ggt	acc	cag	gta	cag	ctg	cag	cag	tca	gag	gga	432
233	Lys	Leu	Ser	Ser	Gly	Thr	Gln	Val	Gln	Leu	Gln	Gln	Ser	Glu	Gly		
234																140	
236	ggc	gtg	gtc	cag	cct	ggg	agg	tcc	ctg	aga	ctc	tcc	tgt	gca	gcg	tct	480
237	Gly	Val	Val	Gln	Pro	Gly	Arg	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	
238																160	
240	gga	tcc	acc	tcc	agt	agc	tat	ggc	atg	aac	tgg	gtc	cgc	cag	gct	cca	528
241	Gly	Phe	Thr	Phe	Ser	Ser	Tyr	Gly	Met	Asn	Trp	Val	Arg	Gln	Ala	Pro	
242																175	
244	ggg	aag	ggg	ctg	gag	tgg	gtt	tca	tac	att	agt	agt	agt	agt	agt	acc	576
245	Gly	Lys	Gly	Leu	Glu	Trp	Val	Ser	Tyr	Ile	Ser	Ser	Ser	Ser	Ser	Thr	
246																190	
248	ata	tac	tac	gca	gac	tct	gtg	aag	ggc	cga	tcc	acc	atc	tcc	aga	gac	624
249	Ile	Tyr	Tyr	Ala	Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	
250																205	
252	aat	tcc	aag	aac	acg	ctg	tat	ctg	caa	atg	aac	agc	ctg	aga	gcc	gag	672
253	Asn	Ser	Lys	Asn	Thr	Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	
254																220	
256	gac	acg	gct	gtg	tat	tac	tgt	gcg	aga	ggg	cct	ggt	atg	gac	gtc	tgg	720
257	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Arg	Gly	Pro	Gly	Met	Asp	Val	Trp	
258																240	
260	ggc	caa	ggg	acc	acg	gtc	acc	gtc	tcc	tca						750	
261	Gly	Gln	Gly	Thr	Val	Thr	Val	Thr	Val	Ser	Ser						
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265	<210> SEQ ID NO: 6																
266	<211> LENGTH: 250																
267	<212> TYPE: PRT																
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273	1				5				10							15	
276	Glu	Arg	Ala	Thr	Ile	Asn	Cys	Lys	Ser	Ser	Gln	Ser	Val	Leu	Tyr	Ser	
277																30	
280	Ser	Asn	Asn	Lys	Asn	Tyr	Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	
281																45	
284	Pro	Pro	Lys	Leu	Leu	Ile	Tyr	Trp	Ala	Ser	Thr	Arg	Glu	Ser	Gly	Val	
285																60	
288	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	
289	65				70						75					80	

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292 Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln  
293 85 90 95  
296 Tyr Tyr Ser Thr Pro Gln Leu Thr Phe Gly Gly Arg Thr Lys Val Asp  
297 100 105 110  
300 Ile Lys Ser Gly Gly Ser Thr Ile Thr Ser Tyr Asn Val Tyr Tyr Thr  
301 115 120 125  
304 Lys Leu Ser Ser Ser Gly Thr Gln Val Gln Leu Gln Gln Ser Glu Gly  
305 130 135 140  
308 Gly Val Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser  
309 145 150 155 160  
312 Gly Phe Thr Phe Ser Ser Tyr Gly Met Asn Trp Val Arg Gln Ala Pro  
313 165 170 175  
316 Gly Lys Gly Leu Glu Trp Val Ser Tyr Ile Ser Ser Ser Ser Thr  
317 180 185 190  
320 Ile Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp  
321 195 200 205  
324 Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu  
325 210 215 220  
328 Asp Thr Ala Val Tyr Tyr Cys Ala Arg Gly Pro Gly Met Asp Val Trp  
329 225 230 235 240  
332 Gly Gln Gly Thr Thr Val Thr Val Ser Ser  
333 245 250  
336 <210> SEQ ID NO: 7  
337 <211> LENGTH: 15  
338 <212> TYPE: DNA  
339 <213> ORGANISM: homo sapiens  
341 <220> FEATURE:  
342 <221> NAME/KEY: CDS  
343 <222> LOCATION: (1)..(15)  
344 <223> OTHER INFORMATION: CDR1 region of VH  
347 <400> SEQUENCE: 7 15  
348 agc tat ggc atg aac  
349 Ser Tyr Gly Met Asn  
350 1 5  
353 <210> SEQ ID NO: 8  
354 <211> LENGTH: 5  
355 <212> TYPE: PRT  
356 <213> ORGANISM: homo sapiens  
358 <400> SEQUENCE: 8  
360 Ser Tyr Gly Met Asn  
361 1 5  
364 <210> SEQ ID NO: 9  
365 <211> LENGTH: 51  
366 <212> TYPE: DNA  
367 <213> ORGANISM: homo sapiens  
369 <220> FEATURE:  
370 <221> NAME/KEY: CDS  
371 <222> LOCATION: (1)..(51)  
372 <223> OTHER INFORMATION: CDR2 region of VH

VERIFICATION SUMMARY  
PATENT APPLICATION: US/10/521,109

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Input Set : A:\pto.kd.txt  
Output Set: N:\CRF4\01272005\J521109.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application No  
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date